

**Amendment to the Claims**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

- Claim 1 (currently amended) A method of performing genetic analysis comprising the steps of:
- a) scanning genomic DNA or derivatives therefrom from a plurality of individuals, wherein at least 10,000 bases are scanned, for genetic variants;
  - b) identifying said genetic variants in said genomic DNA or derivatives therefrom that occur in a plurality of individuals;
  - c) for at least said genomic variants that occur in a plurality of individuals, but not all of said at least 10,000 bases, scanning genomic DNA or derivatives therefrom from additional individuals to identify which of said genetic variants occur in said additional individuals; and
  - d) based on the results of step c), identifying blocks of said variants.
- Claim 2 (original) A method as recited in claim 1 further comprising the step of using said blocks of variants in an association study, whereby said blocks of variants are associated with a phenotypic trait.
- Claim 3 (original) The method as recited in claim 2 further comprising the step of diagnosing said phenotypic trait using one or more variants that are in said block.
- Claim 4 (original) The method as recited in claim 2 further comprising the step of using said variants associated with a phenotypic trait to identify a potential drug target.
- Claim 5 (original) The method as recited in claim 4 further comprising the step of using said potential drug target in a small molecule screening process.
- Claim 6 (currently amended) The method as recited in claim 1 wherein said step of scanning genomic DNA or derivatives therefrom comprises the steps of:
- a) forming an array of probes, wherein said array includes a) probes that are complementary to portions of a first sequence of said genomic DNA or derivative

therefrom and b) probes that are complementary to variants of said genomic DNA or derivative therefrom;

b) hybridizing said genomic DNA or derivative therefrom to said array; and

c) identifying where said genomic DNA or derivative therefrom hybridize to said array.

Claim 7 (original) A method as recited in claim 1 wherein said step of scanning genomic DNA comprises the step of sequencing said genomic DNA with a gel based sequencer.

Claim 8 (original) The method as recited in claim 1 wherein said step of scanning genomic DNA comprises the step of sequencing said genomic DNA with a capillary based sequencer.

Claim 9 (original) The method as recited in claim 1 wherein only variants that occur in more than 10% of the said plurality of individuals are used in step c).

Claim 10 (currently amended) The method as recited in claim 1 where said step of scanning genomic DNA to identify which is of said variants occur in additional individuals comprises the steps of:

a) exposing labeled genomic DNA or a derivative thereof corresponding to said additional individuals to a high density array of probes complementary to said variants; and

b) determining where said genomic DNA hybridizes to said high density array, thereby identifying probes that are complementary to said variants that occur in said additional individuals and further, identifying which of said variants occur in said additional individuals.

Claim 11 (currently amended) The method as recited in claim 1 where said step of scanning genetic genomic DNA to identify which is said variants occur in additional individuals comprises the use of an Invader assay.

Claim 12 (currently amended) The method as recited in claim 1 where said step of scanning genetic genomic DNA to identify which is said variants occur in additional individuals comprises the use of a Taqman assay.

Claim 13 (original) The method as recited in claim 1 wherein more than  $1 \times 10^6$  bases are scanned for variants.

Claim 14 (original) The method as recited in claim 1 wherein more than  $1 \times 10^7$  bases are scanned for variants.

- Claim 15 (original) The method as recited in claim 1 wherein more than  $1 \times 10^8$  bases are scanned for variants.
- Claim 16 (original) The method as recited in claim 1 wherein more than  $1 \times 10^9$  bases are scanned for variants.
- Claim 17 (original) The method as recited in claim 1 wherein introns are scanned for variants.
- Claim 18 (original) The method as recited in claim 1 wherein introns and exons are scanned for variants.
- Claim 19 (original) The method as recited in claim 1 wherein more than 10% of all the non-repeat genomic DNA from the organism is scanned for variants.
- Claim 20 (original) The method as recited in claim 1 wherein more than 25% of all the non-repeat genomic DNA from an organism is scanned for variants.
- Claim 21 (original) The method as recited in claim 1 wherein more than 50% of all the non-repeat genomic DNA from an organism is scanned for variants.
- Claim 22 (original) The method as recited in claim 1 wherein more than 75% of all the non-repeat genomic DNA from an organism is scanned for variants.
- Claim 23 (original) The method as recited in claim 1 wherein said variants are single nucleotide polymorphisms.
- Claim 24 (original) The method as recited in claim 2 further comprising the step of using the results of the association study to stratify a patient population in a clinical trial.
- Claim 25 (original) The method as recited in claim 2 further comprising the step of using the results of the association study to stratify patients that respond to a drug from those who do not respond to a drug.
- Claim 26 (original) The method as recited in claim 2 further comprising the step of using the results of the association study to stratify patients that will show toxic response to a drug from patients that will not show toxic response to a drug.